

1  
2 Supplemental Figure S2  
3  
4 (A)  
5 CLUSTAL W (1.83) multiple sequence alignment of cDNAs  
6  
7  
8 Dlf1 ATGTCTTCTG GAGGAGGAGG AGGAGGAGGA GGAGATCGCC ATGGCCCCTA  
9 OsWRKY11.2 ATGTCTTCTG GAGGAGGAGG AGGAGGAGGA GGAGATCGCC ATGGCCCCTA  
10  
11 Dlf1 CCACCAGCAC GGGCACCTCG GCCGCGGCGA AGGCGTGAT TACGTGTACA  
12 OsWRKY11.2 CCACCAGCAC GGGCACCTCG GCCGCGGCGA AGGCGTGAT TACGTGTACA  
13  
14 Dlf1 GCAGCAGCGA CATGGAGAGC TTCTTCTTCA GCCAACCCGG GGGCGTCGGC  
15 OsWRKY11.2 GCAGCAGCGA CATGGAGAGC TTCTTCTTCA GCCAACCCGG GGGCGTCGGC  
16  
17 Dlf1 ATCGGCGGGG GTGGTGGTGG CGTCGTCGGC GCCGGCGGTG CCGACGAGAT  
18 OsWRKY11.2 ATCGGCGGGG GTGGTGGTGG CGTCGTCGGC GCCGGCGGTG CCGACGAGAT  
19  
20 Dlf1 CATGCCGTAC TCCAGCATCA CGGACTACCT GCAGGGGTTA TTGGACCCCT  
21 OsWRKY11.2 CATGCCGTAC TCCAGCATCA CGGACTACCT GCAGGGGTTA TTGGACCCCT  
22  
23 Dlf1 CCGGGCTAGC TCGGCACCTC GACGTGGCGT GCCCGTCGTC TCAGGACACG  
24 OsWRKY11.2 CCGGGCTAGC TCGGCACCTC GACGTGGCGT GCCCGTCGTC TCAGGACACG  
25  
26 Dlf1 GTGGTCAAGC AGGAGCTGTC GGTGGATGTG ACGAGCCACG ACAGCCAGGG  
27 OsWRKY11.2 GTGGTCAAGC AGGAGCTGTC GGTGGATGTG ACGAGCCACG ACAGCCAGGG  
28  
29 Dlf1 CACCGGCGGC GTCGCCGGAG AAGGCGTCGC GCAGGCCACG CCGAACTCGT  
30 OsWRKY11.2 CACCGGCGGC GTCGCCGGAG AAGGCGTCGC GCAGGCCACG CCGAACTCGT  
31  
32 Dlf1 CGGCGTCTTT CTCGTCCAGC GACGGAGAGG CGGAGGGCGG CAAATCGTCA  
33 OsWRKY11.2 CGGCGTCTTT CTCGTCCAGC GACGGAGAGG CGGAGGGCGG CAAATCGTCA  
34  
35 Dlf1 CGCCCGTGCA AGAAGGGTCA GCGAAGGCG GAGGAGGAGG ACGACAAGGA  
36 OsWRKY11.2 CGCCCGTGCA AGAAGGGTCA GCGAAGGCG GAGGAGGAGG ACGACAAGGA  
37  
38 Dlf1 TGAGGAGGAT GGAGAGAACT CCAAGAAACC GAACAAGCCC AAGAAGAAAAG  
39 OsWRKY11.2 TGAGGAGGAT GGAGAGAACT CCAAGAAACC GAACAAGCCC AAGAAGAAAAG  
40  
41 Dlf1 CTGAGAAGAG GCAGCGGCAG CCTCGCGTGG CGTTCCTCAC CAAGAGCGAG  
42 OsWRKY11.2 CTGAGAAGAG GCAGCGGCAG CCTCGCGTGG CGTTCCTCAC CAAGAGCGAG  
43  
44 Dlf1 GTTGATCACC TCGAGGACGG CTACCGGTGG CGCAAGTACG GCCAGAAGGC  
45 OsWRKY11.2 GTTGATCACC TCGAGGACGG CTACCGGTGG CGCAAGTACG GCCAGAAGGC  
46  
47 Dlf1 AGTCAAGAAC AGCCCATACC CGAGGAGCTA CTACCGGTGC ACGACGCCCA  
48 OsWRKY11.2 AGTCAAGAAC AGCCCATACC CGAGGAGCTA CTACCGGTGC ACGACGCCCA  
49  
50 Dlf1 AGTGCGGTGT GAAGAAGCGG GTGGAGCGGT CGTACCAGGA CCCCTCCACG  
51 OsWRKY11.2 AGTGCGGTGT GAAGAAGCGG GTGGAGCGGT CGTACCAGGA CCCCTCCACG  
52  
53 Dlf1 GTGATACCA CGTACGAAGG GCAGCACACG CACCACAGCC CGGCGAGCCT  
54 OsWRKY11.2 GTGATACCA CGTACGAAGG GCAGCACACG CACCACAGCC CGGCGAGCCT  
55  
56 Dlf1 CCGCGGCGGC GCGGCGGCG TCGGCATCGT CGGAGGGCAC CACCACCACC  
57 OsWRKY11.2 -----  
58  
59 Dlf1 ACCTCTTCAT GCCCGGCGTG CATGGCCTGC CGCCGTCGCA CCTCATGCCG  
60 OsWRKY11.2 -----  
61  
62 Dlf1 GCGGGGTTC ACCCTGAGCT GATGGGCTC ATGCACCACC ACCCGGCCAT  
63 OsWRKY11.2 -----  
64  
65 Dlf1 GGCCGCCGCC GCCGCAAACC CTAGCATGTA CTTCCCGGGC GTAGCTGCTT  
66 OsWRKY11.2 ----- GCCGCAAACC CTAGCATGTA CTTCCCGGGC GTAGCTGCTT  
67  
68 Dlf1 CTGCTCCGCC GCCTCCTGCT GTGGCTGGCG GCGGTGCAAT GCCGCCAAC  
69 OsWRKY11.2 CTGCTCCGCC GCCTCCTGCT GTGGCTGGCG GCGGTGCAAT GCCGCCAAC  
70  
71 Dlf1 GATCATCTC CTCTTCAGCA GCATCACTTC ACTGACTACG CCCTGCTGCA  
72 OsWRKY11.2 GATCATCTC CTCTTCAGCA GCATCACTTC ACTGACTACG CCCTGCTGCA  
73  
74 Dlf1 AGACCTTTC CCTTCCACAA TGCCAGCAG CAACCCATGA  
75 OsWRKY11.2 AGACCTTTC CCTTCCACAA TGCCAGCAG CAACCCATGA  
76

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77
78
79 (B)
80 CLUSTAL W (1.83) multiple sequence alignment of proteins
81
82
83 Dlf1      MSSGGGGGGG GDRHGPHYQH  GHLGRGEGAD  YVYSSSDMES  FFFSQPGGVG
84 OsWRKY11.2  MSSGGGGGGG GDRHGPHYQH  GHLGRGEGAD  YVYSSSDMES  FFFSQPGGVG
85
86 Dlf1      IGGGGGGVVG  AGGADEIMPY  SSITDYLQGL  LDPSGLARHL  DVACPSSQDT
87 OsWRKY11.2  IGGGGGGVVG  AGGADEIMPY  SSITDYLQGL  LDPSGLARHL  DVACPSSQDT
88
89 Dlf1      VVKQELSVDV  TSHDSQGTGG  VAGEGVAQAT  PNSSASFSSS  DGEAEGGKSS
90 OsWRKY11.2  VVKQELSVDV  TSHDSQGTGG  VAGEGVAQAT  PNSSASFSSS  DGEAEGGKSS
91
92 Dlf1      RRCKKGQAKA  EEEDDKDEED  GENSKKPNKP  KKKAEKRQRQ  PRVAFLTKSE
93 OsWRKY11.2  RRCKKGQAKA  EEEDDKDEED  GENSKKPNKP  KKKAEKRQRQ  PRVAFLTKSE
94
95 Dlf1      VDHLEDGYRW  RKYGQKAVKN  SPYPRSYRC  TTPKCGVKKR  VERSYQDPST
96 OsWRKY11.2  VDHLEDGYRW  RKYGQKAVKN  SPYPRSYRC  TTPKCGVKKR  VERSYQDPST
97
98 Dlf1      VITTYEGQHT  HHSPASLRGG  GGGVGIVGGH  HHHHLFMPGV  HGLPPSHLMP
99 OsWRKY11.2  VITTYEGQHT  HHSPASRRKP  -----  -----  -----
100
101 Dlf1      AGFHPELMGL  MHHHPAMAAA  AANPSMYFPG  VAASAPPPPA  VAGGGAMPPN
102 OsWRKY11.2  -----  -----  -----  -----  -----
103
104 Dlf1      DHPPLQQHHF  TDYALLQDLF  PSTMPSSNP
105 OsWRKY11.2  -----  -----  -----
106

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